

AMENDMENTS TO THE CLAIMS

1.– 13. (Cancelled)

14. (New) A method of generating a local-global alignment score which indicates a global and a local similarity between a first protein structure and a second protein structure, the method comprising:

receiving a protein structure correspondence wherein a plurality of positions in the protein structure correspondence indicates a corresponding pair of residues in the first protein structure and the second protein structure;

identifying a longest contiguous segment comprising a plurality of contiguous positions in the correspondence, wherein the root mean square deviation of a set of pairs of residues within the segment is less than a specified threshold value;

identifying a global distance metric based on a number of pairs of residues in the correspondence that are within a pre-determined distance of each other;

generating the local-global alignment score based on the longest contiguous segment and the global distance metric; and

storing the local-global alignment score.

15. (New) The method of claim 14, further comprising:

generating a plurality of correspondences for the first protein structure and second protein structure;

generating a plurality of scores based on the plurality of correspondences;

selecting a correspondence from the plurality of correspondences based on the plurality of scores.

16. (New) The method of claim 14, further comprising:

generating a new correspondence based on the number of pairs of residues in the correspondence that are within a pre-defined distance of each other and the longest contiguous segment.

17. (New) The method of claim 14, wherein identifying a longest contiguous segment comprising a plurality of contiguous positions in the correspondence comprises:

determining a plurality of root mean square deviations corresponding to a plurality of sets of pairs of residues at a plurality of contiguous positions in the correspondence, wherein the plurality of root mean square deviations are determined using a plurality of specified threshold values; and
identifying a longest contiguous segment corresponding to a set of pairs of residues of the plurality of pairs of residues based on the plurality of root mean square deviations.

18. (New) The method of claim 14, wherein identifying a global distance metric comprises:
identifying plurality of distance scores, wherein each distance score corresponds to a number of pairs of residues in the correspondence that are within a pre-determined distance of a plurality of pre-defined distances; and
selecting the global distance metric based on the plurality of distance scores.